

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 20:16:46 ; Search time 4913 Seconds
(without alignments)
3136.324 Million cell updates/sec

Title: US-10-616-309-4
Perfect score: 1615
Sequence: 1 MKQLWFAMSLVTGSLIFSAN.....ELPPQTAKRIAENIKFGAAQ 318

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130704_13105/app_query.fasta_1.4
55

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309_CGN_1_1_3731@runat_26042005_130704_13105 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB	ID	Description
No.	Score	Match	Length	DB	ID		
1	1615	100.0	957	6	CQ759953	App1	CQ759953 Sequence
2	1615	100.0	1661	1	ECU37455	X <i>De la aenas</i>	U37455 Escherichia
3	1615	100.0	3192	1	ECU37089	X <i>Raina</i>	U37089 Escherichia
c 4	1615	100.0	10208	1	AE005487	<i>Genome perna</i>	AE005487 Escherich
c 5	1615	100.0	12767	1	AE015278	2002	AE015278 Shigella
c 6	1615	100.0	29254	1	ECOK12RIII		D64044 Escherichia
c 7	1615	100.0	110000	1	U00096_26		Continuation (27 o
c 8	1615	100.0	110000	1	U00096_27		Continuation (28 o
c 9	1615	100.0	270365	1	AP002562	1999 <i>seq</i>	AP002562 Escherich
c 10	1615	100.0	290380	1	AE016987	X	AE016987 Shigella
c 11	1611	99.8	300099	1	AE016764		AE016764 Escherich
12	1465	90.7	13311	1	STAF001386		AF001386 Salmonell
13	1465	90.7	13311	6	AX191732		AX191732 Sequence
c 14	1465	90.7	22108	1	AE008819		AE008819 Salmonell
c 15	1461	90.5	145050	1	AL627275		AL627275 Salmonell
16	1461	90.5	300431	1	AE016835		AE016835 Salmonell
17	1334	82.6	1041	6	AR387875		AR387875 Sequence
18	1066	66.0	1122	6	BD248394		BD248394 Gene part
19	1044	64.6	10886	1	AE013731		AE013731 Yersinia
c 20	1044	64.6	110000	1	BX936398	34	Continuation (35 o
21	1044	64.6	258050	1	AJ414153		AJ414153 Yersinia
22	1044	64.6	290294	1	AE017136		AE017136 Yersinia
23	1041	64.5	4819	1	AY098586		AY098586 Yersinia
c 24	933	57.8	110000	1	BX950851	36	Continuation (37 o
c 25	840	52.0	348505	1	BX571870		BX571870 Photorhab
26	840	52.0	349980	6	AX770909		AX770909 Sequence
27	770.5	47.7	3545	1	PHRRPOE		L41667 Photobacter
28	770.5	47.7	3545	1	PHRRPOEA		L41688 Photobacter
c 29	764.5	47.3	349814	1	CR378673		CR378673 Photobact
30	749	46.4	1020	6	AR378439		AR378439 Sequence
c 31	739.5	45.8	12162	1	AE004316		AE004316 Vibrio ch
c 32	698.5	43.3	248650	1	AP005341		AP005341 Vibrio vu
33	698.5	43.3	300732	1	AE016802		AE016802 Vibrio vu
c 34	673	41.7	296650	1	AP005082		AP005082 Vibrio pa
35	603	37.3	106645	6	CQ873068		CQ873068 Sequence
36	600	37.2	10631	1	U32746		U32746 Haemophilus
37	600	37.2	110000	6	BD426631	06	Continuation (7 of
38	600	37.2	110000	6	AR274513	06	Continuation (7 of
39	600	37.2	110000	6	AR541453	06	Continuation (7 of
40	587.5	36.4	110000	1	AE016827	21	Continuation (22 o
c 41	585.5	36.3	11975	1	AE006215		AE006215 Pasteurel
42	351.5	21.8	10058	1	AE015578		AE015578 Shewanell
43	336.5	20.8	5000	1	AB189022		AB189022 Shewanell

	44	293.5	18.2	301995	1	AE016779
c	45	269.5	16.7	1855	6	CQ872495

AE016779	Pseudomon
CQ872495	Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 20:03:17 ; Search time 610 Seconds
(without alignments)
3086.029 Million cell updates/sec

Title: US-10-616-309-4
Perfect score: 1615
Sequence: 1 MKQLWFAMSLVTGSLIFSAN.....ELPPQTAKRIAENIKFGAAQ 318

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130704_13093/app_query.fasta_1.4
55

-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309_@CGN_1_1_470_@runat_26042005_130704_13093 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04: *
1: geneseqn1980s: *
2: geneseqn1990s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *

WO 2002/094867

11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1615	100.0	957	12	ADH45224	Adh45224 Enterobac
2	1334	82.6	1041	11	ACH98809	Ach98809 Klebsiell
3	1066	66.0	1122	3	AAZ98342	Aaz98342 A. thalia
4	851	52.7	1968	5	AAS82067	Aas82067 DNA encod
5	840	52.0	957	10	ACF71993	Acf71993 Photorhak
6	840	52.0	110000	10	ACF67367_51	Continuation (52 o
7	840	52.0	110000	10	ACF67367_52	Continuation (53 o
8	840	52.0	110000	10	ACF65387_3	Continuation (4 of
9	749	46.4	1020	10	ADF03160	Adf03160 Bacterial
10	603	37.3	106645	13	ADT05645	Adt05645 Haemophil
11	600	37.2	110000	2	AAT42063_06	Continuation (7 of
c 12	321	19.9	1986	5	AAS92912	Aas92912 DNA encod
c 13	317.5	19.7	2180	5	AAS93271	Aas93271 DNA encod
c 14	269.5	16.7	1855	13	ADT05072	Adt05072 Haemophil
15	255	15.8	1065	11	ABD14466	Abd14466 Pseudomon
c 16	255	15.8	1308	11	ABD14265	Abd14265 Pseudomon
17	255	15.8	1800	2	AAQ70238	Aaq70238 P. aerugi
18	255	15.8	1800	2	AAQ70237	Aaq70237 P. aerugi
19	255	15.8	1800	3	AAA51920	Aaa51920 P. aerugi
20	163	10.1	100	8	ACD79772	Acd79772 E. coli K
21	160	9.9	100	8	ACD79771	Acd79771 E. coli K
22	157	9.7	100	8	ACD79770	Acd79770 E. coli K
23	127.5	7.9	342	6	ABN75321	Abn75321 Human ORF
24	109	6.7	19342	4	AAS59534	Aas59534 Propionib
25	109	6.7	19342	8	ACF64463	Acf64463 Propionib
26	104.5	6.5	1635	8	ACA41299	Aca41299 Prokaryot
27	104.5	6.5	1635	10	ABZ38409	Abz38409 N. gonorr
28	103	6.4	3459	8	ACA37296	Aca37296 Prokaryot
29	103	6.4	110000	10	ADF77343_04	Continuation (5 of
30	101.5	6.3	1170	13	ADS56280	Ads56280 Bacterial
31	101	6.3	3282	11	ABD06652	Abd06652 Pseudomon
c 32	101	6.3	4158	11	ABD06744	Abd06744 Pseudomon
33	101	6.3	4953	11	ABD06623	Abd06623 Pseudomon
c 34	100.5	6.2	1374	8	ACA26695	Aca26695 Prokaryot
35	100.5	6.2	1641	2	AAZ11996	Aaz11996 Neisseria
36	98	6.1	1995	8	ACA23302	Aca23302 Prokaryot
37	96	5.9	1494	11	ABD16357	Abd16357 Pseudomon
c 38	96	5.9	1509	11	ABD16065	Abd16065 Pseudomon
39	96	5.9	15272	4	ABL03697	Abl03697 Drosophil
40	95.5	5.9	1221	6	ABN68595	Abn68595 Streptoco
41	95.5	5.9	1224	8	ACA50778	Aca50778 Prokaryot
42	95	5.9	14391	13	ADS96571	Ads96571 Drosophil
43	95	5.9	46593	3	AAA81456	Aaa81456 N. mening
44	95	5.9	110000	3	AAA81489_5	Continuation (6 of

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 23:02:11 ; Search time 203 Seconds
(without alignments)
2563.232 Million cell updates/sec

Title: US-10-616-309-4
Perfect score: 1615
Sequence: 1 MKQLWFAMSLVTGSLIFSAN.....ELPPQTAKRIAENIKFGAAQ 318

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130705_13155/app_query.fasta_1.4
55

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309 @CGN_1_1_69 @runat_26042005_130705_13155 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				ID	Description
	No.	Score	Match	Length DB		
	1	1334	82.6	1041	4	US-09-489-039A-4604 X
	2	749	46.4	1020	4	US-09-543-681A-3445 X
	3	600	37.2	1830121	4	US-09-557-884-1 <i>Itac</i>
	4	600	37.2	1830121	4	US-09-643-990A-1 <i>HGS</i>
	5	255	15.8	1065	4	US-09-252-991A-13070
c	6	255	15.8	1308	4	US-09-252-991A-12869
	7	255	15.8	1800	1	US-08-260-202A-10
	8	255	15.8	1800	1	US-08-017-114-10
	9	255	15.8	1800	3	US-08-505-307-10
	10	255	15.8	1800	3	US-09-609-151A-10
	11	255	15.8	1800	5	PCT-US94-02034-10
	12	102.5	6.3	2112	4	US-09-902-540-3277
c	13	102.5	6.3	17480	4	US-09-902-540-1151
	14	101	6.3	3282	4	US-09-252-991A-5256
c	15	101	6.3	4158	4	US-09-252-991A-5348
	16	101	6.3	4953	4	US-09-252-991A-5227
	17	96	5.9	1494	4	US-09-252-991A-14961
c	18	96	5.9	1509	4	US-09-252-991A-14669
	19	93.5	5.8	16423	4	US-09-902-540-1120
c	20	93	5.8	11563	4	US-09-902-540-1019
	21	93	5.8	246444	4	US-09-949-016-13113
	22	92	5.7	2256	4	US-09-902-540-6853
c	23	92	5.7	4302	4	US-09-902-540-576
c	24	92	5.7	9146	4	US-09-902-540-990
	25	91	5.6	1830	4	US-09-252-991A-3563
c	26	91	5.6	1926	4	US-09-252-991A-3531
	27	90.5	5.6	830	4	US-09-593-887-5
	28	90	5.6	1668	4	US-09-252-991A-15085
	29	90	5.6	3288	4	US-09-107-532A-201
	30	90	5.6	11647	4	US-09-949-016-12059
	31	90	5.6	11648	4	US-09-949-016-13801
	32	89.5	5.5	2172	1	US-07-982-712-1
	33	89.5	5.5	536165	4	US-09-214-808-1
	34	89	5.5	1245	3	US-09-242-050-1
	35	89	5.5	2036	4	US-09-949-016-2059
	36	88.5	5.5	1575	4	US-09-252-991A-3100
c	37	88.5	5.5	4859	3	US-09-453-702B-154
c	38	88.5	5.5	5536	4	US-09-902-540-803
	39	88	5.4	1530	4	US-09-252-991A-13672
	40	88	5.4	1815	4	US-09-252-991A-7621
c	41	88	5.4	1932	4	US-09-252-991A-7931
	42	88	5.4	2925	4	US-09-252-991A-7069
c	43	88	5.4	4185	3	US-08-961-527-173
	44	88	5.4	5523	4	US-09-902-540-3952
c	45	88	5.4	5658	4	US-09-647-344A-17

*diagnoses
Therapeutics*


```
Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
```

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1615	100.0	957	19	US-10-616-309-3	Sequence 3, Appli
2	1066	66.0	1122	16	US-10-342-224-75	Sequence 75, Appli
3	600	37.2	1830121	17	US-10-329-670-1	Sequence 1, Appli
4	600	37.2	1830121	18	US-10-158-865-1	Sequence 1, Appli
5	127.5	7.9	342	11	US-09-864-408A-535	Sequence 535, App
6	106	6.6	855	15	US-10-156-761-4327	Sequence 4327, Ap
c 7	106	6.6	9025608	15	US-10-156-761-1	Sequence 1, Appli
8	105	6.5	1745	18	US-10-767-701-13257	Sequence 13257, A
9	104.5	6.5	1635	17	US-10-282-122A-29169	Sequence 29169, A
10	103	6.4	3459	17	US-10-282-122A-25166	Sequence 25166, A
c 11	102.5	6.3	2603	18	US-10-425-115-58128	Sequence 58128, A
12	101.5	6.3	1170	17	US-10-369-493-31954	Sequence 31954, A
c 13	100.5	6.2	1374	17	US-10-282-122A-14565	Sequence 14565, A
14	98.5	6.1	2357	17	US-10-424-599-19556	Sequence 19556, A
15	98	6.1	1995	17	US-10-282-122A-11172	Sequence 11172, A
16	97.5	6.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
17	96	5.9	1275	18	US-10-437-963-62362	Sequence 62362, A
18	95.5	5.9	637	17	US-10-424-599-75055	Sequence 75055, A
19	95.5	5.9	1224	17	US-10-282-122A-38648	Sequence 38648, A
20	95.5	5.9	1224	18	US-10-474-792-119	Sequence 119, App
21	95.5	5.9	3066	15	US-10-156-761-1742	Sequence 1742, Ap
22	95.5	5.9	3511	18	US-10-437-963-51948	Sequence 51948, A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 27, 2005, 20:23:46 ; Search time 3680 Seconds
(without alignments)
3289.249 Million cell updates/sec

Title: US-10-616-309-4
Perfect score: 1615
Sequence: 1 MKQLWFAMSLVTGSLIFSAN.....ELPPQTAKRIAENIKFGAAQ 318

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10616309/runat_26042005_130705_13115/app_query.fasta_1.4
55

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10616309 @CGN_1_1_3437 @runat_26042005_130705_13115 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	335	20.7	535	9	CL667196	CL667196 PRI0154b_
	2	316	19.6	798	9	CL679590	CL679590 PRI0126c_
c	3	315.5	19.5	552	8	AQ990079	AQ990079 Rfc00790
	4	119	7.4	650	8	BZ367313	BZ367313 id03f12.b
	5	110	6.8	828	8	BZ559729	BZ559729 pacs2-164
c	6	98.5	6.1	794	9	CG448483	CG448483 OGTCB40TV
c	7	98	6.1	711	9	CL860410	CL860410 OR_CBa009
	8	98	6.1	2095	3	CNS0A1PU	BX830564 Arabidops
	9	97.5	6.0	1857	3	AK080782	AK080782 Mus muscu
	10	97.5	6.0	3830	3	AK031181	AK031181 Mus muscu
	11	97	6.0	890	5	BU188866	BU188866 AGENCOURT
c	12	97	6.0	1068	4	BG423398	BG423398 602449239
	13	97	6.0	1149	4	BG246201	BG246201 602359102
	14	96.5	6.0	380	7	CN252855	CN252855 EST018791
	15	96.5	6.0	560	7	CN250672	CN250672 EST016597
	16	96.5	6.0	782	6	CD576521	CD576521 UCRPT01_0
	17	96.5	6.0	871	6	CD574232	CD574232 UCRPT01_0
	18	96	5.9	3386	3	AK046666	AK046666 Mus muscu
	19	95.5	5.9	612	7	CN244788	CN244788 EST010667
	20	95	5.9	800	8	BZ401449	BZ401449 EINDF04TF
c	21	95	5.9	838	8	BZ391409	BZ391409 EINBH65TR
	22	94	5.8	515	6	CA375958	CA375958 654186 NC
c	23	93.5	5.8	493	2	BF651566	BF651566 274381 MA
	24	93.5	5.8	516	6	CB065020	CB065020 px86h04.y
	25	93	5.8	682	4	BJ235699	BJ235699 BJ235699
c	26	93	5.8	703	9	CE102856	CE102856 tigr-gss-
	27	93	5.8	737	7	CK656702	CK656702 3017HAEMU
	28	92.5	5.7	763	5	BX090614	BX090614 BX090614
c	29	92.5	5.7	822	3	CNS08PKF	BX022555 Single re
	30	92.5	5.7	853	6	CA280028	CA280028 SCVPLB2C0
	31	92	5.7	595	9	CE127506	CE127506 tigr-gss-
	32	92	5.7	616	6	CD082980	CD082980 MA3-9999U
c	33	92	5.7	633	7	CN911036	CN911036 021119ABM
	34	92	5.7	664	6	CD082227	CD082227 MA3-9999U
	35	92	5.7	704	6	CD079868	CD079868 MA3-9999U
	36	92	5.7	722	6	CD835383	CD835383 BN45.045F
c	37	92	5.7	861	6	CB316085	CB316085 AGENCOURT
c	38	92	5.7	976	5	BU849602	BU849602 AGENCOURT
	39	92	5.7	988	5	BQ961211	BQ961211 AGENCOURT
	40	92	5.7	1788	9	CL973619	CL973619 OsIFCC024
c	41	91.5	5.7	632	4	BJ799561	BJ799561 BJ799561
c	42	91.5	5.7	869	4	BI660875	BI660875 603303929
	43	91.5	5.7	1506	3	AK078318	AK078318 Mus muscu
c	44	91	5.6	685	7	CK976531	CK976531 4108010 B
c	45	91	5.6	689	7	CK977911	CK977911 4109407 B

ALIGNMENTS